In the Specification:

Please amend the paragraph beginning on page 12, line 12 as follows:

--This alignment of several MinD amino acid sequences in Fig. 1 from various photosynthetic organisms was performed using CLUSTAL W 1.8. The alignment revealed regions of high sequence similarity, indicating that the gene has been highly conserved during the evolution of chloroplasts. The MinD protein encoded by *AtMinD1* shares a 65% identity with the MinD protein from *Chlorella vulgaris* (P56346), a slightly lower extent of identity (58-62%) with the MinD proteins encoded in the plastid genomes of *Guillardia theta* (AAC35621), *Prototheca wickerhamii* (CAB53105), *Nephroselmis olivacea* (AAD54908) and *Oryza sativa* (AF149810), and a 53% identity with the MinD protein from the photosynthetic prokaryote *Synechocystis* (PCC6803, Q55900). AtMinD also shares a greater than 40% amino acid identity with the bacterial MinD sequences of *Bacillus subtilis* (Q01464); *Escherichia coli* (BAA36022); *Helicobacter pylori* 26695 (AAD07400); *Deinococcus radiodurans* (AAF10331); and *Aquifex aeolicus* (AAC06996), data not shown. Sequence identity was calculated using the SIM local alignment algorithm. (Huang and Miller 1991) with the default parameters specified on the ExPASy Molecular Biology Server, Swiss Institute of BioInformatics ~~(http://expasy.hcuge/sprot/sim-prot.html)~~. --

Please amend the paragraph beginning at page 14, line 3 as follows:

The MZF18 clone (AB009056) was obtained from the *Arabidopsis* Biological Research Center in Columbus, Ohio. The region corresponding to the *AtminD1* ORF was amplified from MZF18 with Deep Vent Polymerase (New England BioLab) using the following primers: forward primer, 5'-CCGAATTCGAAGCAGCAGCACTATCAATGG-3' (SEQ ID NO:5); reverse primer 5'-CGGAATTCGATCCGTTTGCCATTTAGCC-3' (SEQ ID NO:6). Both primers incorporated recognition sites for *Eco*RI. The PCR product was sequenced in its entirety to ensure that no mutations had been introduced, and ligated in both orientations into pBluescript (Stratagene). The plasmid with the 5' end of the insert nearest the T3 promoter was designated KG405; the plasmid with 5' end of the insert nearest the T7 promoter was designated KG406. The plasmids were maintained in a *minCDE* deletion strain of *E. coli,* RC3F. For the transgenic constructs, the *Eco*RI-restricted PCR fragment was ligated into the *Eco*RI cloning site of pART7 behind the CaMV 35S promoter in either the sense or antisense orientation. The transgenes were then excised from the resulting plasmids with *NotI* and ligated into the *NotI* cloning site in the binary transformation vector pART27,

yielding plasmids KG402 containing the *AtMinD1* antisense construct, and KG404 containing the *AtMinD1* sense construct. Both transformation vectors also included a selectable marker from pART27 conferring plant resistance to kanamycin.